

We claim:

1. A substantially purified nucleic acid molecule of the *Myxococcus xanthus* genome having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1850 through SEQ ID NO: 9691 and complements thereof.

5 2. The substantially purified nucleic acid molecule according to claim 1, having a BLASTX Bit Score of at least 100.

3. The substantially purified nucleic acid molecule according to claim 1, having a GeneMark Probability Score of at least 0.6

10 4. The substantially purified nucleic acid molecule according to claim 1, having a BLASTX Bit Score of at least 100 and a GeneMark Probability Score of at least 0.6.

5. The substantially purified nucleic acid molecule according to claim 1, having a GeneMark Probability Score of at least 0.75.

6. The substantially purified nucleic acid molecule according to claim 1, having a BLASTX Bit Score of at least 150.

7. The substantially purified nucleic acid molecule according to claim 1, having a BLASTX Bit Score of at least 150 and a GeneMark Probability Score of at least 0.75.

8. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule further comprises nucleic acid sequences comprising one or more of a promoter region or regulatory region or parts of said regions.

20 9. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a gene identified in Table 2 encoding a protein involved in the production of polyketides.

10. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a gene identified in Table 3 encoding a serine threonine protein  
25 kinase.

11. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a gene identified in Table 4 encoding an antibiotic resistance protein, DNA modification enzyme, sigma factor or nitrate pathway protein.

12. A substantially purified first nucleic acid molecule which is complementary to a second nucleic acid molecule of the *Myxococcus xanthus* genome having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1850 through SEQ ID NO: 9691 and complements thereof, wherein said first nucleic acid molecule and said second nucleic acid molecule hybridize to one another with sufficient stability to remain annealed to one another under at least low stringency conditions of washing with a salt solution having a concentration of about 2.0 X sodium chloride/sodium citrate (SSC) at 50°C.

13. The substantially purified first nucleic acid molecule according to claim 12 wherein said stringency conditions are at least 0.2 X SSC at 50°C.

14. A substantially purified polypeptide having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 9692 through SEQ ID NO: 16825.

15. A substantially purified polypeptide encoded by a nucleic acid sequence which is at least 90% identical to a sequence selected from the group consisting of SEQ ID NO: 1850 through SEQ ID NO: 9691.

16. The substantially purified polypeptide according to claim 15 which is encoded by a nucleic acid sequence which is at least 95% identical to a sequence selected from the group consisting of SEQ ID NO: 1850 through SEQ ID NO: 9691.

17. A transformed cell or organism having an exogenous nucleic acid molecule which comprises:

- (a) a promoter region which functions in said cell or organism to cause the production of a mRNA molecule; which is linked to
- (b) a structural nucleic acid molecule wherein said structural nucleic acid molecule comprises sequence selected from the group consisting of SEQ ID NO: 1850 through SEQ ID NO: 9691 and complements thereof.

18. A transformed cell or organism of claim 17 wherein said nucleic acid molecule in (b) is linked to a 3' untranslated sequence that functions in said cell or organism to cause termination of transcription.

19. The transformed cell or organism according to claim 17 which is selected from the group consisting of a bacterial cell, plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird, fungal cell and fungus and wherein said mRNA encodes a protein in said cell.

20. The transformed cell or organism according to claim 17, wherein said structural nucleic acid molecule is a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand and the transcribed strand specifically hybridizes to an mRNA molecule.

21. A transformed cell or organism having an exogenous nucleic acid molecule, wherein said nucleic acid molecule comprises:

(a) a promoter region which functions in said cell or organism to cause the production of an mRNA molecule wherein said promoter nucleic acid molecule is selected from the group consisting of a promoter located within SEQ ID NO: 1 through SEQ ID NO: 1849 or complements thereof, wherein said promoter is located upstream of a gene having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1850 through SEQ ID NO: 9691; which is linked to

(b) a structural nucleic acid molecule encoding a protein or peptide.

22. A transformed cell or organism of claim 21 wherein said nucleic acid molecule in (b) is linked to a 3' untranslated sequence that functions in said cell or organism to cause termination of transcription.

23. The transformed cell or organism according to claim 21, which is selected from the group consisting of a bacterial cell, plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird, fungal cell and fungus and wherein said mRNA encodes a protein in said cell.

24. A transformed cell or organism having an exogenous nucleic acid molecule which provides for expression of an mRNA which is complementary to and hybridizes to at least part of a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NO: 1850 through SEQ ID NO: 9691 and homologs thereof.

25. A substantially purified oligonucleotide comprising between about 15 and about 100 nucleotides wherein at least 15 of said nucleotides are identical, homologous or complementary to a sequence of consecutive nucleotides within any of SEQ ID NO: 1850 through SEQ ID NO: 9691.

26. The oligonucleotide according to claim 25, comprising in the range of 18 to 50 nucleotide bases, wherein from 18 to 25 of said bases are identical or complementary to an 18-25 bp

segment of a sequence selected from the group consisting of SEQ ID NO: 1850 through SEQ ID NO: 9691.

27. Computer readable medium having recorded thereon at least 100 nucleotide or amino acid sequences which are nucleotide sequences depicted in SEQ ID NO: 1850 through SEQ ID NO: 9691 or complements thereof or oligomers thereof or amino acid sequences depicted in SEQ ID NO: 9692 through SEQ ID NO: 16825.

28. The computer readable medium according to claim 27, having recorded thereon at least 1000 nucleotide or amino acid sequences.

29. A primer pair for amplification of a nucleic acid molecule of SEQ ID NO: 1850 through SEQ ID NO: 9691 wherein each primer in said primer pair comprises at least 15 nucleotides which are identical, homologous or complementary to a sequence of consecutive nucleotides within any of SEQ ID NO: 1850 through SEQ ID NO: 9691.

30. A collection of at least 50 non-identical nucleic acid or peptide molecules wherein said molecules are selected from the group of molecules consisting of

- (a) nucleic acid molecules comprising a nucleic acid sequence of SEQ ID NO: 1850 through SEQ ID NO: 9691 or fragments thereof;
- (b) nucleic acid molecules which are complementary or homologous to a nucleic acid molecule in (a);
- (c) peptide molecules comprising an amino acid sequence of SEQ ID NO: 9692 through SEQ ID NO: 16825
- (d) peptide molecules which are expressed by a nucleic acid molecule which is homologous to a nucleic acid molecule in (a).

31. The collection according to claim 30, comprising at least 100 non-identical nucleic acid or peptide molecules.

32. The collection according to claim 30, comprising at least 500 non-identical nucleic acid or peptide molecules.

33. The collection according to claim 30, comprising at least 1000 non-identical nucleic acid or peptide molecules.

34. The collection according to claim 30, in an array on a solid support.

35. The collection according to claim 30, comprising primer pairs for nucleic acid molecules.

36. A method for determining gene expression comprising
- (a) collecting mRNA from an organism;
  - (b) using said mRNA as a template for producing a quantity of a labeled nucleic acid molecule;
  - 5 (c) contacting said labeled nucleic acid molecule with a collection of purified nucleic acid molecules according to claim 27.
37. The method according to claim 36, wherein said collection of purified nucleic acid molecules comprises at least 1000 non-identical molecules.

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